Microbiology Community Structure in Bioaerosols and the Respiratory Diseases

Cai Jiayu¹, Ren Qiaoqiao¹, Chen Feilong², Lidan Chen³, Wu Jiguo¹, Wu Zhendong¹, Chen Lingyun¹, Rongzhen Liu⁴, Zhang Guoxia^{1*}

¹Department of Environmental Health, Guangdong Provincial Key Laboratory of Tropical Disease Research, School of Public Health, Southern Medical University, Guangzhou, China

²Guangdong Provincial Key Laboratory of Chinese Medicine Pharmaceutics, School of Traditional Chinese Medicine, Southern Medical University, Guangzhou, China

³Department of Laboratory Medicine, General Hospital of Southern Theater Command, PLA, Guangzhou, Guangdong, China

⁴Nan Fang Hospital, Southern Medical University, Guangzhou, China

*Corresponding Author: Zhang Guoxia, Department of Environmental Health, Guangdong Provincial Key Laboratory of Tropical Disease Research, School of Public Health, Southern Medical University, Guangzhou 510515, China, Tel: +86-20-62789126; Fax: 86-20-61648327; E-mail: guoxiazhang@126.com

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Abstract

Bioaerosols are crucial indicators of air pollution and play an instrumental role as risk factors when it comes to the adverse health outcome. Bioaerosols are not self-contained pollutant, but a mixture of different compounds, including bacteria, fungi and virus, etc. While several reviews have focused on the health effect of its single component such as bacteria or fungi on public health, there is a dearth of the review studies community structure of bioaerosols and their impact on physiological change, especially the change in lunge function. Herein, this review sheds a light on community structure in different functional areas, clarifying its relevant risk to public health where respiratory diseases, including coughing, runny nose, irritated eyes or throat, allergic rhinitis, aggravation of asthma and fatigue as well as some infectious diseases such as tuberculosis and Legionnaire's Disease, are particular elaborated. This review will provide some information to adopt accurate and effective control under the circumstances where the medical burden attributes to bioaerosols exposure is spiraling beyond expectation.

Keywords: Bioaerosols; Microbiology; Community structure; Respiratory diseases

1. Introduction

1.1 What is bioaerosol?

Bioaerosols are small, airborne biological material either attached to particulate matter or not. They are ubiquitous in the environment comprised of aerosols originated biologically such as live or dead microorganism and their metabolites, toxins, or fragments that exist widely in the environment [1]. Moreover, biological aerosols account for large of atmospheric aerosols. Approximately 24% atmospheric particles and 5-10% of the total suspended particulate mass were reported to be composed by biological aerosols. Additionally, bioaerosols were estimated to be responsible for approximately 5 to 34% of indoor particulate matter air pollution in an indoor environment [2] where humans spend more than 90% of their time.

1.2 Where does bioaerosol come from?

Changing and remolding differently in different sites and weather conditions as well as human activities, the composition and abundance of atmospheric microbiomes significantly exert an influence on the effect on public health. The bioaerosols in outdoor environments: numerous studies show that bioaerosols can be emitted from terrestrial, soil, forest, and desert dust, agricultural and composting activities, urban areas, wetlands, coastal, and marine environments [3], and different in diverse places even if they belong to same sort. The bioaerosols in indoor environments: sources of bioaerosols in indoor environments are strongly associated with occupants. Not only the microorganisms dwelling on human skin, feces and hair will become a supplement to bioaerosols existing in indoor atmosphere, but also change the original composition of airborne microorganisms. It is such a significant source that one recent study claimed that once occupants changed the microbial communities on surfaces of the dwellings quickly converged with those of the new occupant's skin [4]. Other sources include pets [5], indoor plants [6] and furnishings, such as residential showerheads [7]. Besides, outdoor sources (passing through windows, doors, and ventilation) will also influence the indoor environment [8].

1.3 The impact of bioaerosol on health

Their impacts on public health should not be overlooked for the reason that the higher suspending pathogen may affect human health by inhalation, skin contact and ingestion, inducing both infectious and non-infectious diseases, some infectious diseases such as Q fever, Legionnaire's diseases, Pontiac fever, or non-infectious disease-asthma, allergic rhinitis, bronchitis, atypical conjunctivitis, and organic dust toxic syndrome in various conditions [9] in the form of bioaerosols containing viruses (enteric viruses, including Noro-and rotaviruses, and some respiratory virus such as influenza and coronaviruses), bacteria (staphylococci, legionellae, tuberculous and nontuberculous), bacterial spore formers (Clostridium difficile and Bacillus anthracis) and fungi (Aspergillus, Penicillium, and Cladosporium spp and Stachybotrys chartarum). On the other sense, early exposure to bioaerosols fosters the development of protection against asthma and atopy in children as those children or adults who are not exposed during their infancy often have exacerbation of their airway disease by later exposure [10]. In addition, regular intermittent exposure to airborne biogenic compounds in natural environments offers pleiotropic health benefits by inhibiting the activities of the highly interconnected PI3K/Akt/mTORC1 system to prevent many pathological processes, including cancers, diabetes, inflammation, immunosuppression, and neurodegenerative diseases [11].

Although exposure to some microbes is considered to be beneficial for health, more research is needed to properly assess their potential health hazards, including inter-individual susceptibility, interactions with non-biological agents, and many proven/unproven health effects. Since the importance of bioaerosols and their impact on human health has been recognized, nevertheless, more research is needed to accurately describe their role in the initiation or development of diverse symptoms and diseases.

This paper is a brief overview of the human health effects of atmospheric bacteria and fungi community structure. In line with the international concern about the public health risk of bioaerosols in recent years, herein, the paper mainly discusses the composition of community structure of bioaerosols in different conditions and its potential threatens to public health.

2. Community Structure of Bioaerosols

2.1 The imperative to study community structure of bioaerosol

The impact of bioaerosols on public health has much to do with the community structure of bioaerosols as different community structure determines the characteristics and level of exposure, echoing the wide spectrum of physiological changes resulting from bioaerosols contact. Hence, it is crucial to identify the community structure clearly, classifying its dominant genera to adopt effective measures for health prevention. Since human beings spend most of their time indoors, and when working physically, bodies seem to absorb more bioaerosols, working places naturally becomes hot spot for many researchers to study the correlation between the community structure of bioaerosols exposure and health risk. With the detected concentrations of either Aspergillus fumigatus or total bacteria was above the nation's recommended threshold levels, occupational workers reported to be exposed to higher concentrations of bioaerosol were susceptible to a higher risk of respiratory illness, including hypersensitivity pneumonitis, chronic obstructive pulmonary disease and mucous membrane irritations [12]. The characterization of atmospheric bioaerosols at 9 sites varied spatially over the city of Tijuana, and that levels were highest in the Tijuana River, livestock operations, a landfill and at a water treatment plant, which were closely related to human life [13].

2.2 The community structure in livestock related operations

Among all sorts of working places, the atmospheric microorganisms in livestock related operations, hospitals, subway, composting facility and some water treatment plants gradually grab most researcher's eyeballs due to their capabilities to produce oceans of potential pathogens as well as intimacy with the public. A field study conducted to collect the bacterial and fungal concentrations and dynamics in an egg production facility and its vicinity revealed that the most prominent bacterial species were gram positive around all areas at all times, and Micrococci topped the rank. Fungi types varied among all five stations [14]. On the other sense, when stratifying by age and livestock exposure, a significant difference of nasal microbiome appears between the livestock workers and those without contact, with distinctively abundant microorganisms, including Moraxella, Aerococcus, Lactobacillus, Clostridium XI, Turicibacter, and Strepotococus. Moreover, in a research comparing the genera in the nares samples of workers working in animal-feeding operations with those not, when stratifying by animal type, Corynebacterium and

Staphylococcus were the most abundant genera in the nares, for example, Clostridium sensu stricto was more abundant in the nares of swine workers than others [15].

2.3 The community structure in hospitals

For the exploration in hospitals, bacterial bioaerosol concentrations were higher at larger than those of fungi according to the result analyzing the air samples of different types of wards and operating theaters in hospital [16]. Among the classified genera, *Penicillium spp.*, *Aspergillus spp.*, and *Mucor spp.* were predominant fungi and the abundance of different bacteria followed a sequence as *Micrococcus luteus> Staphylococcus epidermidis> Streptococcus spp.> Diphtheroid spp.> Micrococcus roseus> Bacillus subtilis* in the all samples [16]. Additionally, *Staphylococcus, Propionibacteria, Corynebacteria, Lactobacillus, and Streptococcus spp* accounted for a large proportion in textile holding rooms, which were generally far less diverse than communities recovered from surfaces in patient rooms [17].

2.4 The community structure in other functional areas

Subway, a main travel mode for human, where human skin microbes is the most abundant taxonomic family, such as the Staphylococcus spp. Staphylococcus epidermidis, S. hominis, S. cohnii, S. caprae, and S. haemolyticus [18]. A composting facility, for its part, its predominant bacterial genera were Bacillus, Streptococcus, Staphylococcus, Acinetobacter and Kocuria, posing a potential hazard to air quality related to physical health [19]. By measuring mesophilic bacteria, M+ and M- Staphylococcus, Pseudomonas fluorescens, Actinobacteria, coliform and psychrophilic bacteria, and microscopic fungi, an article comparing the microbial contamination of air in 11 wastewater treatment plants revealed that the microscopic fungi accounted for the largest percentage followed by psychrophilic bacteria and mesophilic bacteria [20]. Interestingly, the study comparing the assemblage of fungal communities in units with visible mold and no visible mold found that the diversity of fungi in units with visible mold was less abundant as it was occupied with the classes Eurotiomycetes, Saccharomycetes, and Wallemiomycetes. In additional, two Cladosporium species, C. sphaerospermum and C halotolerans. were identified the dominant species in colonies of fungi collected from units with visible mold [21]. The situation is different to two places relatively close, by collecting the air samples simultaneously at two sites relatively close in distance from low to high attitude in one mountain, the study revealed that the structure of microbial compositions of both high attitude and suburban site samples were similar-the prime bacteria was Actinobacteria, Firmicutes, and Proteobacteria, and the dominant fugal genre included Ascomycota, Basidiomycota, and Streptophyta, while the abundance of airborne bacteria and fungi were twice than those of suburban site [22].

2.5 Influence of occupants' activities

Something interesting is that even if in the same room, the community structure will change due to occupants' activities. The study evaluating the relationship between bioaerosols concentration and surgical incision size supported that the intraoperative concentration of bacterial and fungal bioaerosols in four operating rooms was distinctively higher than their preoperative concentration. The results disclosed that more concerns were supposed to attach to the consideration of frequent disinfection in operating rooms as gram-positive bacteria and the Penicillium

and Aspergillus fungi –these species are resistant to adverse conditions- prevailed in operating rooms with an increasing incidence of hospital infection [23]. Even some of routine activities may incur increasing opportunistic pathogens, such as flushing. Particle concentrations varied practically after the flush while they remained level across time and distance. Toilets produced aerosol particles when flushed with a large majority of the particles under 0. 3µm in diameter which were recognized as normal flora or infectious organisms causing gastrointestinal diseases. Thus, the ability of toilet flushing to generate pathogenic microorganisms may arouse a wide concern internationally and call for further effective reduction invention [24].

2.6 Weather conditions act as effect factors of community structure shaping

The community structure, to large degree, changes with different weather conditions. It seems like that that the concentration of bacteria was higher than fungi when measuring the composition of an industrial vicinity in South Africa during summer and winter, while both of them were higher in summer season than in winter, and bacteria identified in summer was similar to those identified in in winter- Staphylococcus sp., Bacillus sp., Micrococcus sp., Flavobacterium sp., Klebsiella sp. and Pseudomonas sp. Furthermore, the fungi measured contained Cladosporium spp., Aspergillus spp., Penicillium spp., Fusarium spp. and Alternaria spp. What deserved more concerns was that children seemed to be exposed to a higher concentration level than adults, facing an additional health risk [25]. On heavy rainfall day, the composition of airborne bacteria was significantly influenced by heavy rainfall as the abundances of airborne Propionibacteriaceae always increased after rainfall, whereas Firmicutes, decreased [26]. After constant high heat events, the average amount as well as diversity of bacteria significantly decreased, such as alpha-Proteobacteria, Caulobacteraceae, Sphingomonadaceae, Xanthomonadaceae, while the abundances of sporeforming bacteria, Firmicutes, Bacillales, Bacillaceae, Burkholderiaceae, Rhodocyclaceae, beta-Proteobacteria, markedly increased [27]. Through a long-term observation and comparison, the result indicated that the average concentration of airborne culturable bacteria and fungi differed with various weather conditions, following the order of haze days sunny days hazardous haze days, but decreased once the haze episodes had progressed for a few days while by analyzing hierarchical distribution maps and heatmaps, the dominant bacterial classes detected were Alphaproteobacteria, Actinobacteria as well as Betaproteobacteria, and the major fungal classes were Dothideomycetes, Eurotiomycetes, and Sordariomycetes [28]. Since every community structure invites unique disease spectrum, knowing and exploring its composition and concentration entitles effective prevention.

3. Influence on Public Health

There are abundant living bacteria and residual biological particles in atmosphere, and these will act as a variety of carriers to influence human health and environment, exerting huge influence on social stability. According to one research, the exposure to some frequent microorganisms such as *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Mycoplasma pneumoniae*, *Haemophilus influenzae*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Mycobacterium tuberculosis* can spell wide array of adverse effect: increasing probability of food pollution, deterioration of cosmetics and medicine as well as corrosion of metallic materials for infrastructure, leading to a huge economic losses [29]. The potential hazard caused by bioaerosols depends on their specific pathogenicity and community structure. Sometimes even in the case of strains not identified as opportunistic pathogens can serve as a

source of antibiotic resistance in the environment, thus posing a potential threat to public health [30]. Moreover, the exposure to bioaerosols and chemical components attaching to particular matter lay hard upon the burden of health risk such as lower birth weight, frequent emergency room visit and hospital admission, more premature death and drastic infectious and chronic non-infectious diseases [31].

4. Respiratory Diseases

4.1 Why bioaerosol can invite severe respiratory diseases

From birth, microbes inside buildings seed, colonize, and transiently occupy our bodies, exerting influence on human health through aerosol deposition, surface contact, and human- animal interactions. In fact, bioaerosols can easily enter the respiratory tract, and a small part of them can exacerbate the occurrence and prevalence of infectious diseases which arise from exposure to biological agents by direct (i.e., licking, touching, biting) or/and indirect contact (i.e., cough, sneeze), vector-borne transmission and airborne transmission [32]. Bioaerosols different in mass and structure are succumbed to source, aerosolization, and environmental condition prominent at the site. They can attach to particular matter, and have its aerodynamic as well as antigenic properties altered, strengthening their abilities to penetrating deeper regions of lung to trigger allergic, toxic and infectious responses in exposed individuals, including coughing runny nose, irritated eyes or throat, allergic rhinitis, aggravation of asthma and fatigue [31]. The aerodynamic diameter of less than 2.5 µm may invites severe health risks, playing an important role in the prevalence of both non-infectious and infectious diseases, and a chronic exposure is linked to some deadly chronic disease, such as cancer.

4.2 Respiratory infectious diseases

Among respiratory infectious diseases, tuberculosis and Legionnaire's Disease caused by atmospheric bacteria are ubiquitous. Tuberculosis (TB) is a chronic infectious disease caused by mycobacterium tuberculosis. It can invade many visceral organs, and the pulmonary tuberculosis infection is common. According to statistics, in 1999, one third of the world's population has been infected with tuberculosis. Mycobacterium tuberculosis found in the lung or larynx of the TB patients is transmitted via droplet nuclei expectorated from those infected persons during coughing, sneezing, and talking [33-34]. The other epidemic disease, Legionnaire's Disease, is primarily spread via inhalation of contaminated aerosols arising from man-made water systems and devices such as showers, whirlpool spas, and cooling towers [35]. The presence of sediments, nutrients, heterotrophic biofilms, and amoebas in warm water, combined with inadequate microbicide treatment, can lead to legionella accumulation. These microorganisms are then atomized in a spray or mist produced by the tower [36]. These susceptible individuals inhaling these Legionella-containing aerosols are at risk of developing Legionnaire's Disease [37].

On the other sense, a research which assessed the fungal diversity and mycotoxigenic fungi in cooling towers revealed that the most prevalent isolated fungi belonged to genera *Aspergillus* and *Penicillium*, and those biological aerosols originating from water-distribution systems can lead to allergic reactions (i.e., asthma, skin allergies, keratitis) and various respiratory problems, or fungal infections via direct contact of water with skin or wounds and inhalation [38].

4.3 Non-infectious respiratory diseases

Biological aerosols are also responsible for some non-infectious allergic diseases, such as asthma. It has been reported that more than 40% of the developed world population has allergies to biological and abiotic environmental agents, and 300 million people worldwide suffer from asthma. Studies on airway microbiota have indicated that microbial dysbiosis, what causes wheezing, chronic bronchitis and the reduction of respiratory function, may associated with prevalence and severity of asthma [39]. However, early-life exposure to lung microbiota might contribute to pulmonary tolerance, which might create a permissive milieu for lung metastasis [40]. A study on the relationship between farm living and childhood asthma shown that farm-related microbial exposure has protective effects on childhood asthma [41]. Infantile exposure can reduce the incidence of childhood asthma not only because the infant's pulmonary flora is not yet fully formed, but also the microbiota in the infant breathing zone (IBZ) differ in absolute quantitative and compositional terms from that of the adult breathing zone (ABZ). Micrococcus and Oxalobacteraceae gen have the richest relative abundance in the IBZ and ABZ, however, the fungal and bacterial concentrations were always higher in the IBZ compared to ABZ [42]. The main mode of movement for infants is crawling, a behavior that can stir up coarse-mode particles (> 1 µm in aerodynamic diameter), microbes, pollen, and allergens from the resuspending floor dust [43] and thus create a concentrated and localized cloud of microbial content around the infant.

Among the domestic aeroallergen exposure, fungal aerosols that mainly come from outdoor air flows and indoor humidity and water damaged items (i.e., carpets, ceilings, and walls), are the dominant source in domestic environment [44]. They can produce mycotoxins, leading to diverse health effects (i.e., weaken immune systems, allergies or irritation, many identifiable diseases, and even death) via ingestion, inhalation as well as dermal contact [45].

4.4 Respiratory diseases of occupational exposure

To be mentioned that occupational exposure to distinct bioaerosols community aggravates the incidence of both infectious and non-infectious diseases. A number of studies, focusing mainly on small-scale family farming, have linked bioaerosol emissions to the potentially fatal disease, Farmer's Lung-the prototype of hypersensitivity pneumonitis, also known as extrinsic allergic alveolitis [46]. This is mainly on account of the fact that agricultural bioaerosols contain bacteria from sources such as bedding, feed and livestock (i.e., manure, skin, allergens and dander) that can provoke inflammation and reduce lung function, leading to a wide range of acute and chronic airway diseases [47-48].

5. Conclusions

In conclusion, findings from studies cited in this review made it clear that even if bioaerosol is a complex heterogeneous mix of distinct biological materials that can enter into body by means of inhalation, ingestion and dermal contact, spelling a chain of adverse health effects in humans. Its microbiology community structure is culpable for the various health outcomes observed in humans. This implies that health effects not only owe to single adverse effect led by particular pathogen, but also combined effect among pathogens in one community regulated by

surroundings. Baring the association between microbiology community structure and respiratory diseases is instrumental in calling for personalized, systematic and accurate prevention to rein in prevalence of pathogens in function areas, frequent outbreak of infectious diseases and the rocketing medical payment, and thereby prolong human lives. Moreover, with the information provided in this paper, comprehensive policies are entitled to enact precise standard guidelines for the biological constituents rather than the total mass of atmospheric matter. To be mentioned that there were few studies reviewing the information about community structure in different function areas, which means many deep-seated reasons await further exploration. In addition, more studies are needed to pay more attention to community structure and better understand the contribution of the joint action among atmospheric microorganisms to pin health-end points down.

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